present invention fulfills this long-standing need and desire in the art.

SUMMARY OF THE INVENTION

The present invention demonstrates an application of the molecular recognition theory, which is the generation of therapeutic agents that may be used to treat disease. Using this approach, a series of complementary peptides for the pro-gly-pro sequence were designed, synthesized, and tested as antagonists of the PMN chemoattractant, N-acetyl-PGP.

In an embodiment of the present invention, there is provided a pharmaceutical composition for ophthalmologic uses. Specifically, such composition is a complementary peptide which comprises complementary sequences to proline-glycine-proline (PGP). Generally, the complementary sequences are designed based on the possible coding triplet for proline and glycine and on the hydropathic value of the two amino acids. Enhancement of the potency of the complementary sequence was achieved with a

multimerization process. The resulting molecule can be divided into 4 specific subunits, connected by amide bonds with different functions: 1) recognition subunit 2) core multimerizing subunit 3) spacer subunit and 4) R N-terminal subunit.

The recognition subunit: the complementary sequence to Pro-Gly-Pro, this subunit is responsible for the interaction with the chemoattractant. The recognition subunit is present as a single unit in the monomer, is repeated twice in the dimer, 4 times in the tetramer and 8 times in the octamer. It is defined by the sequence all-L Arg-Thr-Arg and by the sequence all-L Xxx-Thr-Arg (Xxx = the 20 natural amino acids), and by all-D Arg-Thr-Arg and all-D Xxx-Thr-Arg (Xxx = the 20 natural amino acids).

The core multimerizing subunit, absent from the linear monomers, is characterized by a branching di-amino amino acid (lysine, di-amino propionic acid, di-amino butyric acid) connected to a single alanine, where both amino groups are involved in an amide bond. The function of the core is to determine the number of recognition units in the molecule and to control the relative spatial distribution of the recognition subunits. The core also represents the connection point to the resin during Solid Phase Peptide Synthesis.

The octameric core is defined by the formula all-L $(((B)_2B)_2)$B-Ala, the tetramer by all-L $(B)_2$B-Ala and the dimer by all-L B-Ala (where B= lysine, di-amino propionic acid and di-amino butyric acid). The core was also obtained with all-D amino acids with the same generic formulas.

The spacers represent the connection point between the core and the recognition subunits and determines the relative spatial distribution of the recognition subunits. It can be constituted by a di-glycine. The di-glycine could be substituted by a single amino acid with the formula: $NH_2[CH_2]_n$-COOH [n=2[3-amino propionic acid];3;4;5;6;or 7[8-amino caprylic acid]]

R –terminal subunit: A free amino terminal group on each recognition subunit is not necessary for the subunit function. This group can be functionalized by an R molecule to modify the pharmaco-dynamic properties of the molecule and to produce a more constrained molecule. The R can be H_3C-$(CH_2)_n$-CO with n=0 (acetyl), n=4 (caproyl) and n=14 (palmitoleyl). R can also be the amino acid cysteine. In the case of the tetrameric peptide the sulfur groups could be used for the formation of an intra molecular di-sulfide bridge, generating a constrained bi-cyclic molecule.